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FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 9 July 2003 (20030709/ED)

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L88 ANSWER 1 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1996:556811 BIOSIS
DN PREV199699279167
TI Quality control of DNA sequencing templates and contig **assembly** using quantitative DNA fiber mapping (QDFM) facilities parallelism in producing sequencing.
AU Wang, M. (1); Ericsson, C.; Martin, C.; **Collins, C. (1)**; Palazzolo, M.; **Gray, J. W. (1)**; Weier, H.-U. G. (1)
CS (1) Resource Mol. Cytogenet., Life Sci. Div., Univ. California, Lawrence Berkeley Natl. Lab., Berkeley, CA 94720 USA
SO American Journal of Human Genetics, (1996) Vol. 59, No. 4 SUPPL., pp. A314.
Meeting Info.: **46th Annual Meeting of the American Society of Human Genetics** San Francisco, California, USA October 29-November 2, 1996
ISSN: 0002-9297.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
General Biology - Information, Documentation, Retrieval and Computer Applications 00530
Genetics and Cytogenetics - Human *03508
Mathematical Biology and Statistical Methods *04500
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines 10052
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Replication, Transcription, Translation *10300
Biophysics - Molecular Properties and Macromolecules *10506
Metabolism - Nucleic Acids, Purines and Pyrimidines *13014
BC Hominidae *86215
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Mathematical Biology (Computational Biology); Metabolism; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Miscellaneous Descriptors
GENE EXPRESSION; HUMAN GENOME; MARKERS; **MEETING ABSTRACT**; **MEETING POSTER**; MOLECULAR GENETICS
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
Hominidae (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L88 ANSWER 2 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1996:100562 BIOSIS
DN PREV199698672697
TI A statistical method for the analysis of comparative genomic hybridization

their own but 1996

profiles.
AU Mohapatra, Gavatry (1); Moore, Dan (1); Sudar, Damir (1); Pinkel, Dan (1); **Gray, Joe (1)**; Feuerstein, Burt
CS (1) Div. Mol. Cytometry, Dep. Lab. Med., UCSF, San Francisco, CA 94143 USA
SO Cancer Genetics and Cytogenetics, (1995) Vol. 84, No. 2, pp. 151.
Meeting Info.: **Sixth International Workshop on Chromosomes in Solid Tumors** Tucson, Arizona, USA February 19-21, 1995
ISSN: 0165-4608.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Mathematical Biology and Statistical Methods *04500
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Neoplasms and Neoplastic Agents - Biochemistry *24006
Neoplasms and Neoplastic Agents - Carcinogens and Carcinogenesis *24007
BC Hominidae *86215
IT Major Concepts
Biochemistry and Molecular Biophysics; Cell Biology; Genetics; Mathematical Biology (Computational Biology); Oncology (Human Medicine, Medical Sciences)
IT Miscellaneous Descriptors
CANCER GENETICS; DNA COPY NUMBER; **MEETING ABSTRACT**; STATISTICAL METHOD
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L88 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1995:528155 BIOSIS
DN PREV199598542455
TI Quantitative DNA fiber mapping.
AU Weier, H.-U. G. (1); Wang, M.; Mullikin, J. C.; Zhu, Y.; Cheng, J.-F.; Greulich, K. M.; Bensimon, A; **Gray, J. W.**
CS (1) Cent. Molecular Cytogenetics, Life Sci. Div., MS 74-157, Univ. California, Lawrence Berkeley Lab., 1 Cyclotron Rd., Berkeley, CA 94720 USA
SO Human Molecular Genetics, (1995) Vol. 4, No. 10, pp. 1903-1910.
ISSN: 0964-6906.
DT Article
LA English
AB The assembly of sequence ready, high-resolution physical maps and construction of minimally overlapping contigs for the human as well as model genomes requires accurate determination of the extent of overlap between adjacent clones as well as their relative orientation. This is presently done by procedures such as clone fingerprinting, Southern blot analysis or clone **end sequencing**. We present a complementary analytical technique to map directly cloned DNA sequences on to individual stretched DNA molecules. This approach uses the hydrodynamic force of a receding meniscus to prepare straight high molecular weight DNA molecules that provide a linear template of apprx 2.3 kb/mu-m on to which the cloned probes can be mapped by in situ hybridization. This technique has numerous advantages such as a very high density of mapping templates, reproducible stretching of the mapping template providing a linear genomic scale, determination of clone orientation and direct visualization of DNA repeats. The utility and accuracy of quantitative DNA fiber mapping are illustrated through three examples: (i) mapping of lambda DNA restriction

fragments along linearized apprx 49 kb long lambda phage DNA molecules with apprx 1 kb precision; (ii) localization of the overlap between a cosmid and a colinear P1 clone; and (iii) mapping of P1 clones along a apprx 490 kb yeast artificial chromosome (YAC) with apprx 5 kb precision and estimation of the apprx 25 kb gap between them.

CC Methods, Materials and Apparatus, General - Photography *01012
Cytology and Cytochemistry - Plant *02504
Genetics and Cytogenetics - Plant *03504
Radiation - Radiation and Isotope Techniques *06504
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
External Effects - Pressure *10606
Genetics of Bacteria and Viruses *31500
Virology - Bacteriophage *33504

BC Siphoviridae 02710
Fungi - Unspecified *15000

IT Major Concepts
Biochemistry and Molecular Biophysics; Cell Biology; Equipment, Apparatus, Devices and Instruments; Genetics; Methods and Techniques; Microbiology; Physiology; Radiology (Medical Sciences)

IT Miscellaneous Descriptors
FLUORESCENCE IN-SITU HYBRIDIZATION; HYDRODYNAMIC FORCE; LAMBDA DNA RESTRICTION FRAGMENTS; QUANTITATIVE IMAGE ANALYSIS; YEAST ARTIFICIAL CHROMOSOME

ORGN Super Taxa
Fungi - Unspecified: Fungi, Plantae; Siphoviridae: Viruses

ORGN Organism Name
fungi (Fungi - Unspecified); Siphoviridae (Siphoviridae)

ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants; viruses

L88 ANSWER 4 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1995:476706 BIOSIS
DN PREV199598491006
TI Statistical method for testing genetic gain or loss in CGH profiles.
AU Magrane, G. G.; Moore, D. H. Ii; Cronin, J. E.; Yu, L. C.; Pinkel, D.; **Gray, J. W.**
CS DMC/MCB 230, Box 0808, Univ. Calif., San Francisco, CA 94103-0808 USA
SO American Journal of Human Genetics, (1995) Vol. 57, No. 4 SUPPL., pp. A72.
Meeting Info.: **45th Annual Meeting of the American Society of Human Genetics** Minneapolis, Minnesota, USA October 24-28, 1995
ISSN: 0002-9297.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Mathematical Biology and Statistical Methods 04500
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Neoplasms and Neoplastic Agents - General *24002
Neoplasms and Neoplastic Agents - Carcinogens and Carcinogenesis *24007
BC Hominidae *86215
IT Major Concepts
Cell Biology; Genetics; Oncology (Human Medicine, Medical Sciences)
IT Miscellaneous Descriptors
CHROMOSOME; COMPARATIVE GENOMIC HYBRIDIZATION; DNA; **MEETING ABSTRACT; MEETING POSTER**

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

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L90 ANSWER 1 OF 1 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1987:414134** BIOSIS
DN **BR33:83812**
TI AUTOMATED QUANTIFICATION OF THE FREQUENCY OF ABERRANT CHROMOSOMES IN HUMAN CELLS.
AU LUCAS J; LOZES C; MULLIKIN J; PINKEL D; **GRAY J**
CS LAWRENCE LIVERMORE NATL. LAB., LIVERMORE, CALIF. 94550.
SO XIITH INTERNATIONAL **MEETING** OF THE SOCIETY FOR ANALYTICAL CYTOLOGY, CAMBRIDGE, ENGLAND, UK, AUGUST 9-15, 1987. CYTOMETRY. (1987) 0 (SUPPL 1), 13.
CODEN: CYTODQ. ISSN: 0196-4763.
DT **Conference**
FS BR; OLD
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520**
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Mathematical Biology and Statistical Methods *04500
Radiation - Radiation Effects and Protective Measures *06506
Blood, Blood-Forming Organs and Body Fluids - Blood, Lymphatic and Reticuloendothelial Pathologies *15006
Blood, Blood-Forming Organs and Body Fluids - Lymphatic Tissue and Reticuloendothelial System *15008
BC Hominidae 86215
IT Miscellaneous Descriptors
ABSTRACT LYMPHOBLASTOID CELLS GAMMA-RAYS

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L92 ANSWER 1 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2002:386802** BIOSIS
DN **PREV200200386802**
TI Genomic copy number changes in mouse primary breast tumors and their metastases identified using comparative genomic hybridization to DNA microarrays.
AU Hodgson, Graeme (1); Tirone, Jamie; Malek, Tiffany; Hariono, Sujatmi; Pinkel, Daniel; Albertson, Donna G.; Muller, William J.; **Gray, Joe W.**
CS (1) University of California, San Francisco, San Francisco, CA USA
SO **Proceedings of the American Association for Cancer Research Annual Meeting**, (March, 2002) Vol. 43, pp. 292. print.
Meeting Info.: **93rd Annual Meeting of the American Association for Cancer Research** San Francisco, California, USA April 06-10, 2002
ISSN: 0197-016X.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Cytology and Cytochemistry - Animal *02506
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Animal *03506

Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Respiratory System - Physiology and Biochemistry *16004
Reproductive System - Physiology and Biochemistry *16504
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
BC Muridae 86375
IT Major Concepts
Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics); Tumor Biology
IT Parts, Structures, & Systems of Organisms
breast: reproductive system; chromosome 1: locus p32-36; chromosome 15; chromosome 19; chromosome 2; chromosome 4; chromosome 6; lung: respiratory system; mammary epithelial cell: reproductive system
IT Diseases
genomic copy number abnormality: genetic disease; primary breast tumor: neoplastic disease, reproductive system disease/female
IT Chemicals & Biochemicals
ErbB-2: activation, expression, mutation, phosphorylation; NBL-1; genome; k-Ras; tumor necrosis factor receptor
IT Methods & Equipment
DNA microarray: analytical method; comparative genomic hybridization: analytical method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
mouse (Muridae)
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates

L92 ANSWER 2 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2002:159019** BIOSIS
DN **PREV200200159019**
TI High-resolution assessment of DNA loss in RIP-Tag mouse pancreatic tumors using comparative genomic hybridization to DNA microarrays.
AU Hodgson, Graeme (1); Hager, Jeff; **Collins, Colin**; Wernick, Meredith; Werhane, Heather; Albertson, Donna; Pinkel, Daniel; Hanahan, Douglas; **Gray, Joe**
CS (1) UCSF Cancer Center, San Francisco, CA USA
SO Cytometry Supplement, (2000) No. 10, pp. 179. print.
Meeting Info.: **The XX Congress of the International Society for Analytical Cytology** Montpellier, France May 20-25, 2000 International Society for Analytical Cytology
. ISSN: 1046-7386.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Endocrine System - Pancreas *17008
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
BC Muridae 86375
IT Major Concepts
Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics); Tumor Biology

IT Parts, Structures, & Systems of Organisms
chromosome-16; chromosome-9
IT Diseases
insulinoma: endocrine disease/pancreas, neoplastic disease
IT Chemicals & Biochemicals
DNA
IT Alternate Indexing
Insulinoma (MeSH)
IT Methods & Equipment
comparative genomic hybridization: genetic method; comparative genomic hybridization to DNA microarray: genetic method
IT Miscellaneous Descriptors
loss of heterozygosity; **Meeting Abstract**
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
mouse (Muridae): RIP-Tag
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates

L92 ANSWER 3 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2002:158601** BIOSIS
DN **PREV200200158601**
TI High-resolution assessment of DNA loss in RIP-Tag mouse pancreatic tumors using comparative genomic hybridization to DNA microarrays.
AU Hodgson, Graeme (1); Hager, Jeff (1); **Collins, Colin (1)**; Wernick, Meredith (1); Werhane, Heather (1); Pinkel, Daniel (1); Hanahan, Douglas (1); **Gray, Joe (1)**; Albertson, Donna
CS (1) University of California Cancer Center, San Francisco, CA USA
SO Cytometry Supplement, (2000) No. 10, pp. 60. print.
Meeting Info.: **The XX Congress of the International Society for Analytical Cytology** Montpellier, France May 20-25, 2000 International Society for Analytical Cytology
. ISSN: 1046-7386.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - General *10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Endocrine System - General *17002
Endocrine System - Pancreas *17008
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
BC Muridae 86375
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Methods and Techniques; Tumor Biology
IT Parts, Structures, & Systems of Organisms
chromosome 16: deletion; chromosome 9: deletion; pancreatic islet beta cell: endocrine system
IT Diseases
insulinoma: endocrine disease/pancreas, neoplastic disease
IT Chemicals & Biochemicals
DNA: copy number, high-resolution assessment, loss, microarray; SV40 large T-antigen
IT Alternate Indexing
Insulinoma (MeSH)
IT Methods & Equipment

comparative genomic hybridization: assessment method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
mouse (Muridae): RIP-Tag, model, transgenic
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates

L92 ANSWER 4 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2002:158568** BIOSIS
DN **PREV200200158568**
TI Oligonucleotide-array-based comparative genomic hybridization.
AU Baldocchi, Russ (1); Kowbel, Dave (1); **Collins, Colin (1)**; Glynne, Richard; Tom, Ed; Mack, David; **Gray, Joe**
CS (1) Cancer Center, University of California at San Francisco, San Francisco, CA USA
SO Cytometry Supplement, (2000) No. 10, pp. 50. print.
Meeting Info.: **The XX Congress of the International Society for Analytical Cytology** Montpellier, France May 20-25, 2000 International Society for Analytical Cytology
. ISSN: 1046-7386.
DT **Conference**
LA English
CC **General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520**
Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
IT Major Concepts
Genetics; Methods and Techniques; Tumor Biology
IT Diseases
breast cancer: neoplastic disease, reproductive system disease/female; ovarian cancer: neoplastic disease, reproductive system disease/female
IT Chemicals & Biochemicals
DNA; oligonucleotide
IT Alternate Indexing
Breast Neoplasms (MeSH); Ovarian Neoplasms (MeSH)
IT Methods & Equipment
PCR [polymerase chain reaction]: DNA amplification, amplification method, in situ recombinant gene expression detection, sequencing techniques; oligonucleotide-array-based comparative genomic hybridization: assessment method
IT Miscellaneous Descriptors
genomic copy number: abnormality; **Meeting Abstract**

L92 ANSWER 5 OF 9 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **2002:158546** BIOSIS
DN **PREV200200158546**
TI Technical approaches for producing and analyzing DNA microarrays.
AU Hamilton, Greg (1); **Gray, Joe (1)**; Albertson, Donna (1); Pinkel, Dan (1); Jones, Arthur; Uber, Don; Davy, Donn; Hansen, Tony; Nordmeyer, Robert; Wilson, Dave; Jaklevic, Joe
CS (1) UCSF Cancer Center, San Francisco, CA USA
SO Cytometry Supplement, (2000) No. 10, pp. 43. print.
Meeting Info.: **The XX Congress of the International Society for Analytical Cytology** Montpellier, France May 20-25, 2000 International Society for Analytical Cytology

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FILE COVERS 1907 - 15 Jul 2003 VOL 139 ISS 3
FILE LAST UPDATED: 14 Jul 2003 (20030714/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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L117 ANSWER 1 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN 2003:524409 HCAPLUS
TI End-sequence profiling: Sequence-based analysis of aberrant genomes
AU Volik, Stanislav; Zhao, Shaying; Chin, Koei; Brebner, John H.; Herndon, David R.; Tao, Quanzhou; Kowbel, David; Huang, Guiqing; Lapuk, Anna; Kuo, Wen-Lin; Magrane, Gregg; de Jong, Pieter; Gray, Joe W.; Collins, Colin
CS Cancer Research Institute, University of California Comprehensive Cancer Center, San Francisco, CA, 94115, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(13), 7696-7701
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 13, 14
AB Genome rearrangements are important in evolution, cancer, and other diseases. Precise mapping of the rearrangements is essential for identification of the involved genes, and many techniques have been developed for this purpose. End-sequence profiling (ESP) is now shown to be particularly well suited to this purpose. ESP is accomplished by constructing a bacterial artificial chromosome (BAC) library from a test genome, measuring BAC end sequences, and mapping end-sequence pairs onto the normal genome sequence. Plots of BAC end-sequences d. identify copy no. abnormalities at high resoln. BACs spanning structural aberrations have end pairs that map abnormally far apart on the normal genome sequence. These pairs can then be sequenced to det. the involved genes and breakpoint sequences. ESP anal. of the breast cancer cell line MCF-7 demonstrated its utility for anal. of complex genomes. End sequencing of .apprx.8000 clones (0.37-fold haploid genome clonal coverage) produced a comprehensive genome copy no. map of the MCF-7 genome at better than 300-kb resoln. and identified 381 genome breakpoints, a subset of which was verified by fluorescence in situ hybridization mapping and sequencing. The sequences reported in this paper have been deposited in the GenBank/EMBL/DDBJ database with accession nos. BZ597614-BZ612944 and AC116668. [This abstr. record is one of four records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].
ST end sequence profiling aberrant genome analysis; breast cancer MCF7 genome analysis end sequence profiling
IT Genomic library
(BAC; end-sequence profiling for sequence-based anal. of aberrant genomes as applied to the breast cancer cell line MCF-7)
IT Genetic methods
(ESP (end-sequence profiling); end-sequence profiling for sequence-based anal. of aberrant genomes as applied to the breast cancer cell line MCF-7)
IT Animal cell line

530774-48-2, GenBank BZ600980 530774-49-3, GenBank BZ600981
530774-50-6, GenBank BZ600982 530774-51-7, GenBank BZ600983
530774-52-8, GenBank BZ600984 530774-53-9, GenBank BZ600985
530774-54-0, GenBank BZ600986 530774-55-1, GenBank BZ600987
530774-56-2, GenBank BZ600988 530774-57-3, GenBank BZ600989
530774-58-4, GenBank BZ600990 530774-59-5, GenBank BZ600991
530774-60-8, GenBank BZ600992 530774-61-9, GenBank BZ600993
530774-62-0, GenBank BZ600994 530774-63-1, GenBank BZ600995
530774-64-2, GenBank BZ600996 530774-65-3, GenBank BZ600997
530774-66-4, GenBank BZ600998 530774-67-5, GenBank BZ600999
530774-68-6, GenBank BZ601000
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; end-sequence profiling for sequence-based anal. of aberrant genomes as applied to the breast cancer cell line MCF-7)

L117 ANSWER 5 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN **2002:755055** HCAPLUS
DN **137:258485**
TI Methods for diagnosing and monitoring ovarian cancer by profiling associated marker genes using comparative genomic hybridization array
IN Chin, Koei; Kuo, Wen-lin; Pinkel, Daniel; Albertson, Donna; **Collins, Colin; Gray, Joe W.**
PA USA
SO U.S. Pat. Appl. Publ., 24 pp.
CODEN: USXXCO
DT Patent
LA English
IC ICM C12Q001-68
NCL 435006000
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 14
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2002142305	A1	20021003	US 2001-819103	20010327
WO 2002077292	A1	20021003	WO 2002-US9804	20020326

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI US 2001-819103 A 20010327
AB This invention pertains to the discovery that an amplification of some genes or an increase in that gene activity and a deletion of some genes or a decrease in that gene activity is a marker for the presence of, progression of, or predisposition to, a cancer (e.g., ovarian cancer). Using this information, this invention provides methods of detecting a predisposition to cancer in an animal. The methods involve (i) providing a biol. sample from an animal (e.g. a human patient); (ii) detecting the level of the genes of the present invention within the biol. sample; and (iii) comparing the level of one or more of said genes with a level of one or more of said genes in a control sample taken from a normal, cancer-free tissue. In particular, array comparative genomic hybridization using 5'-amino-linked degenerate oligonucleotide primer (DOP) PCR is used to analyze gene amplification or deletion assocd. ovarian cancer. Approx. twenty amplified or deleted (with >0.4% fold gain or loss of expression at mRNA level) genomic regions with ref. GenBank nos. are identified to be assocd. with human ovarian tumors. Gene-specific arrays targeted to these

ovarian tumor-assocd. markers are described for diagnosis, drug screening and therapy applications.

ST ovary cancer marker gene profiling microarray comparative genomic hybridization; drug screening therapy diagnosis ovary cancer marker gene profiling

IT Primers (nucleic acid)
Probes (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(5'-amino-linked degenerate oligonucleotide primer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Cyclins
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(A, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ADRA1C; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(AF-4, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ATF4, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT DNA microarray technology
(CGH (comparative genomic hybridization); methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Cadherins
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(E-, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(ERBB2, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(Evi-1, increased expression in ovary cancer; methods for diagnosing

and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(FGR, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(FKHR, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(GLUT2, increased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(HTR2A, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT EST (expressed sequence tag)
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(Hs.14518, related gene decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(INSR, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(LPL, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(RARA, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(REV3L; methods for diagnosing and monitoring ovarian cancer by

profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(RGS, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(SST, increased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Transcription factors
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(TBP (TATA box-binding protein), decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(TCL1 (T cell leukemia/lymphoma 1), decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(THRA, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(TOP2A, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(TP53, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Therapy
(adjuvant, for ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Recombination, genetic
(amplification, of ovary cancer marker; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT mRNA
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(assocd. with ovary cancer, detection of the level of; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Diagnosis
(cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Mutation
(deletion, of ovary cancer marker; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Neoplasm
(diagnosis; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Animal tissue
Blood plasma
Blood serum
Cerebrospinal fluid
Saliva
(diagnostic sample; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Antisense oligonucleotides
Ribozymes
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(for antitumor agent screening; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Blood analysis
Urine analysis
(for diagnosis; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chemotherapy
Hormone replacement therapy
Immunotherapy
Radiotherapy
Surgery
(for ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(fyn, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Adrenoceptors
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene ADRA1C, .alpha.1C, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene ATF4, TAXREB67 protein, , decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene FKHR, forkhead protein; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Platelet-derived growth factors
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene PDGFB, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT neu (receptor)
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene c-erbB2, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Transcription factors
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene myb, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chromosome
(human 1, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chromosome
(human 13, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chromosome
(human 14, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chromosome
(human 16, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chromosome
(human 17, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chromosome
(human 19, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chromosome
(human 22, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chromosome
(human 3, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT Chromosome
(human 4, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using

comparative genomic hybridization array)
IT Chromosome
(human 6, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Chromosome
(human 8, ovary cancer marker gene located at; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Antitumor agents
DNA sequences
Drug screening
Gene dosage
Nucleic acid hybridization
Ovary, neoplasm
Protein sequences
Susceptibility (genetic)
cDNA sequences
(methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Cheek
(mucosa, scraping, for diagnosis; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Animal cell
(of ovary cancer, hyperproliferative; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Genetic markers
Tumor markers
(of ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Gene expression profiles, animal
(ovary cancer assocd.; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Cat (Felis catus)
Cattle
Dog (Canis familiaris)
Horse (Equus caballus)
Human
Lagomorpha
Mouse
Nonhuman primate
Swine
(ovary cancer diagnosis in; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Transcription factors
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(repressors, for antitumor agent screening; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Cytotoxic agents
(screening for; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)
IT Proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(solurshin, gene RGS, decreased expression in ovary cancer; methods for

diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT 5-HT receptors
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(type 5-HT2A, gene HTR2A, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT 115926-52-8, Phosphatidylinositol 3-kinase
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene PIK3CA, increased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT 243664-63-3, DNA polymerase .zeta.
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene REV3L, decreased expression in ovary cancer; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT 139805-78-0, GenBank M19722 140027-89-0, GenBank M15024 140035-35-4, GenBank M12783 140035-45-6, GenBank J00306 144915-65-1, GenBank X57830 151066-51-2, GenBank D25235 164498-19-5, GenBank T79768 184512-11-6, GenBank U69961 252820-17-0, GenBank S82592 384442-63-1, GenBank X51688 384451-31-4, GenBank M10051 384463-70-1, GenBank M11730 384528-20-5, GenBank L13773 384597-53-9, GenBank X82240 389182-08-5, GenBank M14333 389182-26-7, GenBank Y00479 389185-22-2, GenBank M15856 391523-84-5, GenBank D90209 391530-10-2, GenBank J04088 391535-27-6, GenBank Z13009 391548-90-6, GenBank Z29090 392043-30-0, GenBank AF032885 398095-16-4, GenBank X06614 398425-77-9, GenBank M55654 412112-08-4, GenBank Z13009
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

IT 212216-75-6, GenBank AF078695
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; methods for diagnosing and monitoring ovarian cancer by profiling assocd. marker genes using comparative genomic hybridization array)

L117 ANSWER 6 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN 2002:555682 HCAPLUS
DN 137:104752
TI Probes to repeat sequence-free genomic regions for use in high throughput screening of genomes
IN **Collins, Colin; Volik, Stanislav V.; Gray, Joe W.**; Albertson, Donna G.; Pinkel, Daniel
PA The Regents of the University of California, USA
SO PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 20
FAN.CNT 1
PATENT NO. KIND DATE APPLICATION NO. DATE

PI	WO 2002057481	A2	20020725	WO 2002-US365	20020107
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2003022166	A1	20030130	US 2001-766450	20010119
PRAI	US 2001-766450	A	20010119		

AB The present invention provides a rapid, efficient, and automated method for identifying unique sequences within the genome. This invention involves the identification of repeat sequence-free subregions within a genomic region of interest as well as the detn. of which of those repeat sequence-free subregions are truly unique within the genome. Once the truly unique subregions are identified, primer sequences are generated that are suitable for the amplification of sequences, e.g., for use as probes or array targets, within the unique subregions.

ST oligonucleotide probe repeat sequence free human genome; primers non repeat sequence genome screening

IT Sequence homology analysis
(BLAST, repeat sequences identified using; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT DNA microarray technology
(CGH, probes for; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT Computer program
(Repeat Masker or Primer 3 software, repeat sequences identified using; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT Optical imaging devices
(displaying oligonucleotide sequence on; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT Human
(genome; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT Nucleic acid hybridization
(in situ, fluorescence, non-repeat sequence probes for; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT Databases
(nucleotide sequence; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT Fluorescent substances
(probe labeled with; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT DNA sequences
Genome
Nucleic acid hybridization
(probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT Repetitive DNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)

(probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(to non-repeat sequences of genome; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

IT 443371-12-8 443371-13-9 443371-14-0 443371-15-1 443371-16-2
443371-17-3 443371-18-4 443371-19-5 443371-20-8 443371-21-9
443371-22-0 443371-23-1 443371-24-2 443371-25-3 443371-26-4
443371-27-5 443371-28-6 443371-29-7 443371-30-0 443371-31-1
443371-32-2 443371-33-3 443371-34-4 443371-35-5 443371-36-6
443371-37-7 443371-38-8 443371-39-9 443371-40-2 443371-41-3
443371-42-4 443371-43-5 443371-44-6 443371-45-7 443371-46-8
443371-47-9 443371-48-0 443371-49-1 443371-50-4 443371-51-5
443371-52-6 443371-53-7 443371-54-8 443371-55-9 443371-56-0
443371-57-1 443371-58-2 443371-59-3 443371-60-6 443371-61-7
443371-62-8 443371-63-9 443371-64-0 443371-65-1 443371-66-2
443371-67-3 443371-68-4 443371-69-5 443371-70-8 443371-71-9
443371-72-0 443371-73-1 443371-74-2 443371-75-3 443371-76-4
443371-77-5 443371-78-6 443371-79-7 443371-80-0 443371-81-1
443371-82-2 443371-83-3 443371-84-4 443371-85-5 443371-86-6
443371-87-7 443371-88-8 443371-89-9 443371-90-2 443371-91-3
443371-92-4 443371-93-5 443371-94-6 443371-95-7 443371-96-8
443371-97-9 443371-98-0 443371-99-1 443372-00-7 443372-01-8
443372-02-9 443372-03-0 443372-04-1 443372-05-2 443372-06-3
443372-07-4 443372-08-5 443372-09-6 443372-10-9 443372-11-0
443372-12-1 443372-13-2 443372-14-3 443372-15-4 443372-16-5
443372-17-6 443372-18-7 443372-19-8 443372-20-1 443372-21-2
443372-22-3 443372-23-4
RL: PRP (Properties)
(unclaimed sequence; probes to repeat sequence-free genomic regions for use in high throughput screening of genomes)

L117 ANSWER 7 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:895110 HCAPLUS
DN 138:366457
TI Genome scanning with array CGH delineates regional alterations in mouse islet. [Erratum to document cited in CA136:353395]
AU Hodgson, Graeme.; Hager, Jeffrey H. H.; **Volik, Stas.**; Hariono, Sujatmi.; Wernick, Meredith.; Moore, Dan.; Nowak, Norma.; Albertson, Donna G.; Pinkel, Daniel; **Collins, Colin**; Hanahan, Douglas; **Gray, Joe W.**
CS Cancer Genetics and Breast Oncology Programs, UCSF Cancer Center, University of San Francisco at San Francisco, San Francisco, CA, 94143-0808, USA
SO Nature Genetics (2001), 29(4), 491
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America Inc.
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 3
AB The name of the seventh author, Norma Nowak (Department of Human Genetics, Roswell Park Cancer Institute, Buffalo, new York 14263, USA), was omitted from the author list.
ST erratum mouse pancreas tumor genome copy number; carcinoma mouse chromosome alteration LOH9 LOH16 erratum; microarray comparative genomic hybridization genome copy number erratum
IT Nucleic acid hybridization
(DNA-DNA, CGH (comparative genomic hybridization); delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH,

and identification of corresponding human genes (Erratum))
IT Gene, animal
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FSTL1, PPP2R3, CDKNIB, STMN1, PFDN4 and CYP24; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT Pancreatic islet of Langerhans, neoplasm
(carcinoma; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT Gene dosage
(changes in; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT DNA microarray technology
Genome
Human
Loss of heterozygosity
Mouse
Mutation
(delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT Chromosome
(mouse 14; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT Chromosome
(mouse 16, LOH16 region; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT Chromosome
(mouse 2; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT Chromosome
(mouse 4; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT Chromosome
(mouse 6; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT Chromosome
(mouse 8; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))
IT Chromosome
(mouse 9, LOH9 region; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes (Erratum))

L117 ANSWER 8 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:894920 HCAPLUS
DN 136:353395
TI Genome scanning with array CGH delineates regional alterations in mouse islet carcinomas
AU Hodgson, Graeme; Hager, Jeffrey H.; **Volik, Stas**; Hariono, Sujatmi; Wernick, Meredith; Moore, Dan; Albertson, Donna G.; Pinke, Daniel; **Collins, Colin**; Hanahan, Douglas; **Gray, Joe W.**
CS Cancer Genetics and Breast Onrology Programs, UCSF Cancer Center, University of California at San Francisco, San Francisco, CA, 94143-0808, USA

SO Nature Genetics (2001), 29(4), 459-464
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America Inc.
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 3

AB Carcinomas that develop in the pancreatic islets of transgenic mice expressing the SV40 T-antigens (Tag) under transcriptional control of the rat insulin II promoter (RIP) progress through well-characterized stages that are similar to aspects of human tumor progression, including hyperplastic growth, increased angiogenesis and reduced apoptosis. The latter two stages have been assocd. with recurrent loss of heterozygosity (LOH) and reduced genome copy no. on chromosomes 9 (LOH9) and 16 (LOH16), aberrations which we believe contribute to these phenotypes. Earlier analyses localized LOH9 to approx. 3 Mb and LOH16 to approx. 30 Mb (both syntenic with human 3q21-q25) but were limited by low throughput and a lack of informative polymorphic markers. Here we show that comparative genomic hybridization to DNA microarrays (array CGH) overcomes these limitations by allowing efficient, genome-wide analyses of relative genome copy no. The CGH arrays used in these expts. carried BACs distributed at 2-20-MB intervals across the mouse genome and at higher d. in regions of interest. Using array CGH, we further narrowed the loci for LOH9 and LOH16 and defined new or previously unappreciated recurrent regions of copy-no. decrease on chromosomes 6, 8 and 14 (syntenic with human chromosomes 12p11-p13. 16q24.3 and 13q11-q32, resp.) and regions of copy-no. increase on chromosomes 2 and 4 (syntenic to human chromosomes 20q13.2 and 1p32-p36, resp.). Our analyses of human genome sequences syntenic to these regions suggest that CYP24, PFDN4, STMN1, CDKNIB, PPP2R3 and FSTL1 are candidate oncogenes or tumor-suppressor genes. We also show that irradn. and genetic background influence the spectrum of aberrations present in these tumors.

ST mouse pancreas tumor genome copy number; carcinoma mouse chromosome alteration LOH9 LOH16; microarray comparative genomic hybridization genome copy number

IT Nucleic acid hybridization
(DNA-DNA, CGH (comparative genomic hybridization); delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)

IT Gene, animal
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FSTL1, PPP2R3, CDKNIB, STMN1, PFDN4 and CYP24; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)

IT Pancreatic islet of Langerhans, neoplasm
(carcinoma; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)

IT Gene dosage
(changes in; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)

IT DNA microarray technology
Genome
Human
Loss of heterozygosity
Mouse
Mutation
(delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)

IT Chromosome
(mouse 14; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding

human genes)
IT Chromosome
(mouse 16, LOH16 region; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)
IT Chromosome
(mouse 2; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)
IT Chromosome
(mouse 4; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)
IT Chromosome
(mouse 6; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)
IT Chromosome
(mouse 8; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)
IT Chromosome
(mouse 9, LOH9 region; delineation of chromosomal alterations in mouse islet carcinomas using microarray-CGH, and identification of corresponding human genes)
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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(19) Shi, Y; Cancer 1997, V19, P104 HCAPLUS
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(24) Vainberg, I; Cell 1998, V93, P863 HCAPLUS
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L117 ANSWER 9 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:886543 HCAPLUS
DN 136:1600
TI A novel method to identify rearrangements in a test genome from terminal sequence profiling
IN **Collins, Colin; Volik, Stanislav; Gray, Joe W.**
PA Regents of the University of California, USA
SO PCT Int. Appl., 38 pp.
CODEN: PIXXD2
DT Patent

LA English
IC ICM C12Q
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 14
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001092558	A2	20011206	WO 2001-US17757	20010531
	WO 2001092558	A3	20020404		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

	AU 2001075110	A5	20011211	AU 2001-75110	20010531
PRAI	US 2000-586529	A	20000531		
	WO 2001-US17757	W	20010531		

AB The present invention provides a novel method to identify rearrangements in a test genome, e.g., a tumor genome, when compared to a ref. genome. This method provides major improvements over previous methods in terms of efficiency, rapidity, and cost-effectiveness. Briefly, this method involves generating or obtaining a large insert vector library from a test genome, sequencing the ends of the inserts in the library, and comparing the co-linearity of the sequenced ends in the library with corresponding sequences within a substantially-sequenced ref. genome. This invention is useful for any of a no. of applications, including for identifying rearrangements in tumor genomes and for detg. genetic differences between closely related species as well as between different strains of the same species.

ST human tumor genome rearrangement terminal sequence profiling; bioinformatics computer software terminal sequence profiling

IT Computer program
Genetic vectors
Genomic library
PAC (P1-derived artificial chromosome)
(a novel method to identify rearrangements in a test genome from terminal sequence profiling)

IT Insertion sequence
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(a novel method to identify rearrangements in a test genome from terminal sequence profiling)

IT Neoplasm
(cell, genome of, as test genome; a novel method to identify rearrangements in a test genome from terminal sequence profiling)

IT BAC (bacterial artificial chromosome)
(clones; a novel method to identify rearrangements in a test genome from terminal sequence profiling)

IT Genome
(comparison; a novel method to identify rearrangements in a test genome from terminal sequence profiling)

IT Mutation
(deletion; a novel method to identify rearrangements in a test genome from terminal sequence profiling)

IT Human
(genome, as ref. genome; a novel method to identify rearrangements in a test genome from terminal sequence profiling)

IT Chromosome
(human, ref. genome present on different; a novel method to identify rearrangements in a test genome from terminal sequence profiling)

IT Bioinformatics
(of terminal sequences; a novel method to identify rearrangements in a test genome from terminal sequence profiling)
IT Recombination, genetic
(rearrangement, breakpoint; a novel method to identify rearrangements in a test genome from terminal sequence profiling)
IT Robotics
(sequencing; a novel method to identify rearrangements in a test genome from terminal sequence profiling)
IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(terminal sequence of clones; a novel method to identify rearrangements in a test genome from terminal sequence profiling)
IT Genetic methods
(terminal sequence profiling; a novel method to identify rearrangements in a test genome from terminal sequence profiling)
IT DNA sequence analysis
(terminal sequences; a novel method to identify rearrangements in a test genome from terminal sequence profiling)
IT Recombination, genetic
(translocation; a novel method to identify rearrangements in a test genome from terminal sequence profiling)

L117 ANSWER 10 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:748135 HCAPLUS
DN 135:268157
TI DNA sequence analysis software
IN **Collins, Colin; Volik, Stanislav; Gray, Joe W.**
PA The Regents of the University of California, USA
SO PCT Int. Appl., 40 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G09G005-36
ICS C12Q001-68
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 20
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001075856	A1	20011011	WO 2001-US10399	20010330

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 2000-541438 A 20000331
AB A method and app. for analyzing a DNA sequence visually display important information about a sequence utilizes computer software. The invention discloses a software tool to identify and display repeat information (RepeatMasker), alignment information with sequences from public and proprietary data based, frequency of selected nucleotide pairs, and other information of interest to researchers.
ST computer software genetic method
IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(CpG island; DNA sequence anal. software)

IT Computer program
Computers
DNA sequence analysis
DNA sequences
Databases
Genetic methods
Mouse
Repetitive DNA sequences
Simulation and Modeling, biological
(DNA sequence anal. software)
IT Genetic element
Satellite DNA
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(DNA sequence anal. software)
IT Nucleic acid library
(GSS; DNA sequence anal. software)
IT Repetitive DNA
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(LINE; DNA sequence anal. software)
IT Repetitive DNA
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(SINE; DNA sequence anal. software)
IT DNA sequences
(alignment; DNA sequence anal. software)
IT Repetitive DNA
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(dinucleotide, CpG; DNA sequence anal. software)
IT Computer application
(graphics; DNA sequence anal. software)
IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(long terminal repeat; DNA sequence anal. software)
IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(low complexity region; DNA sequence anal. software)
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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(2) Perlin; US 5876933 A 1999 HCAPLUS

L117 ANSWER 11 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:429888 HCAPLUS
TI Comprehensive genome sequence analysis of a breast cancer amplicon
AU **Collins, Colin**; **Volik, Stanislav**; Kowbel, David; Ginzinger, David; Ylstra, Bauke; Cloutier, Thomas; Hawkins, Trevor; Predki, Paul; Martin, Christopher; Wernick, Meredith; Kuo, Wen-Lin; Alberts, Arthur; **Gray, Joe W.**
CS University of California San Francisco Cancer Center, San Francisco, CA, 94143-0808, USA
SO Genome Research (2001), 11(6), 1034-1042
CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal; Letter
LA English
AB Gene amplification occurs in most solid tumors and is assocd. with poor prognosis. Amplification of 20q13.2 is common to several tumor types including breast cancer. The 1 Mb of sequence spanning the 20q13.2 breast

cancer amplicon is one of the most exhaustively studied segments of the human genome. These studies have included amplicon mapping by comparative genomic hybridization (CGH), fluorescent in-situ hybridization (FISH), array-CGH, quant. microsatellite anal. (QUMA), and functional genomic studies. Together these studies revealed a complex amplicon structure suggesting the presence of at least two driver genes in some tumors. One of these, ZNF217, is capable of immortalizing human mammary epithelial cells (HMEC) when overexpressed. In addn., we now report the sequencing of this region in human and mouse, and on quant. expression studies in tumors. Amplicon localization now is straightforward and the availability of human and mouse genomic sequence facilitates their functional anal. However, comprehensive annotation of megabase-scale regions requires integration of vast amts. of information. We present a system for integrative anal. and demonstrate its utility on 1.2 Mb of sequence spanning the 20q13.2 breast cancer amplicon and 865 kb of syntenic murine sequence. We integrate tumor genome copy no. measurements with exhausive genome landscape mapping, showing that amplicon boundaries are assocd. with maxima in repetitive element d. and a region of evolutionary instability. This integration of comprehensive sequence annotation, quant. expression anal., and tumor amplicon boundaries provide evidence for an addnl. driver gene prefoldin 4 (PFDN4), coregulated genes, conserved noncoding regions, and assoc. repetitive elements with regions of genomic instability at this locus.

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L117 ANSWER 12 OF 19 HCAPLUS COPYRIGHT 2003 ACS

AN **2000:790675** HCAPLUS

DN **133:330496**

TI Comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease

IN **Gray, Joe W.**; Pinkel, Dan; Albertson, Donna G.; **Collins, Colin C.**; Baldocchi, Russell A.
PA The Regents of the University of California, USA
SO PCT Int. Appl., 28 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-68
ICS C12P019-34; C07H021-02; C07H021-04
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 14
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000066779	A1	20001109	WO 2000-US11433	20000428
W: CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6465182	B1	20021015	US 1999-302056	19990429
EP 1173621	A1	20020123	EP 2000-930197	20000428
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI US 1999-302056	A	19990429		
WO 2000-US11433	W	20000428		

AB The present invention provides methods of detg. relative copy no. of target nucleic acid sequences and precise mapping of chromosomal abnormalities assocd. with disease. The methods of the invention use target nucleic acid sequences immobilized on a solid surface, to which a sample comprising two sets of differentially labeled nucleic acid sequences are hybridized. The hybridization of the labeled nucleic acid sequences to the solid surface is then detected using std. techniques.

ST nucleic acid array comparative fluorescence hybridization oligonucleotide probe; disease diagnosis chromosome aberration mapping DNA microarray fluorescence hybridization; tumor diagnosis DNA comparative fluorescence hybridization

IT DNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(COT-1, blocking agent; comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)

IT Chromosome aberrations
Diagnosis
Genetic mapping
Immobilization, biochemical
Indicators
Nucleic acid hybridization
(comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)

IT Nucleic acids
RNA
RL: ANT (Analyte); BUU (Biological use, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)

IT Gene, animal
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with

disease)
IT cDNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
IT mRNA
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
IT Animal tissue
(fetal; comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
IT Embryo, animal
(fetus, tissue of; comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
IT Disease, animal
(genetic; comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
IT Glass beads
RL: NUU (Other use, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(immobilization surface; comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
IT Nucleic acid hybridization
(in situ, fluorescence; comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(labeled, with fluorescent indicator; comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
IT Neoplasm
(nucleic acid from; comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
IT PCR (polymerase chain reaction)
(used to prep. labeled nucleic acid sequences; comparative fluorescence hybridization to oligonucleotide microarrays used for precise mapping of chromosomal abnormalities assocd. with disease)
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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(2) Lisitsyn; Science 1993, V259, P946 HCAPLUS
(3) Pinkel; US 5830645 A 1998 HCAPLUS

L117 ANSWER 13 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN **2000:397353** HCAPLUS
DN **133:291649**
TI Quantitative mapping of amplicon structure by array CGH identifies CYP24 as a candidate oncogene
AU Albertson, Donna G.; Ylstra, Bauke; Segraves, Richard; **Collins,**

Colin; Dairkee, Shanaz H.; Kowbel, David; Kuo, Wen-Lin; **Gray, Joe W.**; Pinkel, Daniel
CS Cancer Research Institute, University of California, San Francisco, San Francisco, CA, USA
SO Nature Genetics (2000), 25(2), 144-146
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America Inc.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 14
AB The authors show here that the quant. measurement of DNA copy no. across amplified regions using array comparative genomic hybridization GCH may facilitate oncogene identification by providing precise information on the locations of both amplicon boundaries and amplification maxima.
ST oncogene map amplicon
IT Gene, animal
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(oncogene; quant. mapping of amplicon structure by array CGH identifies CYP24 as candidate oncogene)
IT Genetic mapping
(quant. mapping of amplicon structure by array CGH identifies CYP24 as candidate oncogene)
IT Amplicon
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(quant. mapping of amplicon structure by array CGH identifies CYP24 as candidate oncogene)
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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L117 ANSWER 14 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN **2000:203128** HCAPLUS
DN **132:330389**
TI Genome changes and gene expression in human solid tumors
AU **Gray, Joe W.; Collins, Colin**
CS UCSF Cancer Center, University of California San Francisco, San Francisco, CA, 94143-0808, USA
SO Carcinogenesis (2000), 21(3), 443-452
CODEN: CRNGDP; ISSN: 0143-3334
PB Oxford University Press
DT Journal; General Review
LA English
CC 3-0 (Biochemical Genetics)
Section cross-reference(s): 14
AB A review, with 141 refs. Genome-wide anal. techniques such as chromosome

painting, comparative genomic hybridization, representational difference anal., restriction landmark genome scanning and high-throughput anal. of LOH are now accelerating high-resoln. genome aberration localization in human tumors. These techniques are complemented by procedures for detection of differentially expressed genes such as differential display, nucleic acid subtraction, serial anal. of gene expression and expression microarray anal. These efforts are enabled by work from the human genome program in phys. map development, cDNA library prodn./sequencing, and genome sequencing. This review covers several commonly used large-scale genome and gene expression anal. techniques, outlines genomic approaches to gene discovery and summarizes information that has come from large-scale analyses of human solid tumors.

ST review genetic technique tumor

IT Genetic methods
Genome
(genome changes and gene expression in human solid tumors)

IT Gene, animal
RL: ADV (Adverse effect, including toxicity); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(genome changes and gene expression in human solid tumors)

IT Chromosome
(human; genome changes and gene expression in human solid tumors)

RE.CNT 142 THERE ARE 142 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

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L117 ANSWER 15 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN **1998:798281** HCAPLUS
DN **130:192338**
TI Genome scanning and gene discovery in breast and ovarian cancer
AU **Gray, Joe W.**; **Collins, Colin**; Pinkel, Daniel;
Shayesteh, Laleh; Lu, Yiling; Mills, Gordon
CS UCSF Cancer Center, University of California, San Francisco, CA, USA
SO Pezcoller Foundation Symposia (1998), 9(Biology of Tumors), 65-72
CODEN: PFSYES; ISSN: 0961-785X
PB Plenum Publishing Corp.
DT Journal; General Review
LA English
CC 3-0 (Biochemical Genetics)
Section cross-reference(s): 14
AB A review, with 26 refs., on the use of comparative genomic hybridization (CGH) to scan breast and ovarian cancers. Recurrent abnormalities were defined in these studies. The authors focused on (1) a region of increased copy no. on chromosome 20q esp. apparent in breast cancers, and (2) a region of increased copy no. at chromosome 3q26 esp. apparent in ovarian cancers.

ST review genome scanning breast ovary cancer
IT Gene dosage
Genome
Ovary, neoplasm
(genome scanning and gene discovery in human breast and ovarian cancer)
IT Chromosome
(human 20; genome scanning and gene discovery in human breast and ovarian cancer)
IT Chromosome
(human 3; genome scanning and gene discovery in human breast and ovarian cancer)
IT Genetics
(hybridization, comparative genomic hybridization; genome scanning and gene discovery in human breast and ovarian cancer)
IT Mammary gland
(neoplasm; genome scanning and gene discovery in human breast and ovarian cancer)
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L117 ANSWER 16 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN **1998:663115** HCAPLUS
DN **130:21094**
TI High resolution analysis of DNA copy number variation using comparative genomic hybridization to microarrays
AU Pinkel, Daniel; Segraves, Richard; Sudar, Damir; Clark, Steven; Poole, Ian; Kowbel, David; **Collins, Colin**; Kuo, Wen-Lin; Chen, Chira; Zhai, Ye; Dairkee, Shanaz H.; Ljung, Britt-marie; **Gray, Joe W.**; Albertson, Donna G.
CS Cancer Genetics Program, UCSF Cancer Center, Univ. California, San Francisco, CA, 94143-0808, USA
SO Nature Genetics (1998), 20(2), 207-211
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal

LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 14
AB Gene dosage variations occur in many diseases. In cancer, deletions and copy no. increases contribute to alterations in the expression of tumor-suppressor genes and oncogenes, resp. Developmental abnormalities, such as Down, Prader Willi, Angelman and Cri du Chat syndromes, result from gain or loss of one copy of a chromosome or chromosomal region. Thus, detection and mapping of copy no. abnormalities provide and approach for assocg. aberrations with disease phenotype and for localizing crit. genes. Comparative genomic hybridization (CGH) was developed for genome-wide anal. of DNA sequence copy no. in a single expt. In CGH, differentially labeled total genomic DNA from a 'test' and a 'ref.' cell population are co-hybridized to normal metaphase chromosomes, using blocking DNA to suppress signals from repetitive sequences. The resulting ratio of the fluorescence intensities at a location on the 'cytogenetic map', provided by the chromosomes, is approx. proportional to the ratio of the copy nos. of the corresponding DNA sequences in the test and ref. genomes. CGH has been broadly applied to human and mouse malignancies. The use of metaphase chromosomes, however, limits detection of events involving small regions (of less than 20 Mb) of the genome, resoln. of closely spaced aberrations and linking ratio changes to genomic/genetic markers. Therefore, more laborious locus-by-locus techniques have been required for higher resoln. studies. Hybridization to an array of mapped sequences instead of metaphase chromosomes could overcome the limitations of conventional CGH (ref. 6) if adequate performance could be achieved. Copy no. would be related to the test/ref. fluorescence ratio on the array targets, and genomic resoln. could be detd. by the map distance between the targets, or by the length of the cloned DNA segments. We describe here our implementation of array CGH. We demonstrate its ability to measure copy no. with high precision in the human genome, and to analyze clin. specimens by obtaining new information on chromosome 20 aberrations in breast cancer.
ST comparative genomic hybridization chromosome aberration human breast cancer
IT Nucleic acid hybridization
(DNA-DNA; high resoln. anal. of DNA copy no. variation using comparative genomic hybridization to microarrays)
IT Genetic methods
(comparative genomic hybridization; high resoln. anal. of DNA copy no. variation using comparative genomic hybridization to microarrays)
IT Chromosome aberrations
Genetic mapping
(high resoln. anal. of DNA copy no. variation using comparative genomic hybridization to microarrays)
IT Chromosome
(human 20; high resoln. anal. of DNA copy no. variation using comparative genomic hybridization to microarrays)
IT Mammary gland
(neoplasm; high resoln. anal. of DNA copy no. variation using comparative genomic hybridization to microarrays)
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L117 ANSWER 17 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN **1992:208828** HCAPLUS
DN **116:208828**
TI Construction and characterization of plasmid libraries enriched in sequences from single human chromosomes
AU **Collins, Colin**; Kuo, Wen Lin; Segraves, Richard; Fuscoe, James; Pinkel, Daniel; **Gray, Joe W.**
CS Biomed. Sci. Div., Lawrence Livermore Natl. Lab., Livermore, CA, 94550, USA
SO Genomics (1991), 11(4), 997-1006
CODEN: GNMCEP; ISSN: 0888-7543
DT Journal
LA English
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 13
AB Plasmid libraries enriched in sequences from single chromosome types have been constructed for all human chromosomes. This was accomplished by transferring inserts from the Charon 21A phage libraries constructed by the National Lab. Gene Library Project into Bluescribe plasmids. Insert material freed by complete digestion of the phage libraries with HindIII or EcoRI was cloned into the corresponding sites in Bluescribe plasmids. The sizes of the Bluescribe library inserts detd. by gel electrophoresis range from near 0 to .apprx.6 kb. Fluorescence in situ hybridization (FISH) with the plasmid libraries showed that all hybridize along both arms of the expected (target) chromosome type with varying intensity. However, the plasmid libraries for chromosomes 1, 4, 9, 11, 16, 18, and 20 hybridize weakly or not at all near the centromeres of the target chromosome types. The libraries for chromosomes 13, 14, 15, 21, and 22 cross-hybridize near the centromeres of all members of this group and hybridize weakly to the short arms of the target chromosomes. FISH with each library allows specific staining of the target chromosome type in metaphase spreads. The signals resulting from FISH with libraries for chromosome 1, 4, 8, 9, 13, 14, 17, 18, 21, and Y are sufficiently intense to permit anal. in interphase nuclei. Examples of the use of these libraries for translocation detection, marker chromosome characterization, and interphase aneuploidy anal. are presented.
ST human chromosome cloning Bluescribe plasmid; fluorescence in situ hybridization human chromosome; plasmid library single human chromosome
IT Plasmid and Episome
(Bluescribe, contg. enriched sequences from single human chromosomes,

construction and characterization of)
IT Interphase, biological
(aneuploidy of, anal. of human, using Bluescribe plasmid libraries enriched in sequences from single chromosome types)
IT Chromosome
(cloning of enriched sequences from single human, in Bluescribe plasmids, anal. of chromosome aberrations subsequent to)
IT Molecular cloning
(of enriched sequences from single human chromosomes, in Bluescribe vectors, chromosome aberration anal. subsequent to)
IT Nucleic acid hybridization
(in situ, fluorescence, in detection of human chromosome aberrations, using Bluescribe plasmid libraries enriched in sequences from single chromosome types)
IT Recombination, genetic
(translocation, detection of human chromosome, using Bluescribe plasmid libraries enriched in sequences from single chromosome types)

L117 ANSWER 18 OF 19 HCAPLUS COPYRIGHT 2003 ACS
AN **1989:547970** HCAPLUS
DN **111:147970**
TI An efficient method for selecting unique-sequence clones from DNA libraries and its application to fluorescent staining of human chromosome 21 using in situ hybridization
AU Fuscoe, James C.; **Collins, Colin C.**; Pinkel, Dan; **Gray, Joe W.**
CS Biomed. Sci. Div., Lawrence Livermore Natl. Lab., Livermore, CA, 94550, USA
SO Genomics (1989), 5(1), 100-9
CODEN: GNMCEP; ISSN: 0888-7543
DT Journal
LA English
CC 3-5 (Biochemical Genetics)
Section cross-reference(s): 13
AB An efficient procedure is described for selecting large nos. of unique-sequence or very low repeat-sequence probes from recombinant phage libraries. Probes were selected from the Charon 21A library LL21NSO2 (made from DNA from human chromosome 21) in a multistep process is in which (1) inserts from LL21NSO2 were subcloned into Blue-scribe plasmids, (2) plasmids were grown at high d. in colonies on nitrocellulose, and (3) plasmids were selected as contg. unique-sequence inserts if DNA from the colonies failed to hybridize, at low stringency, to radiolabeled total human DNA. Thus, 1530 colonies were picked to form the library pBS-U21/1530. About 80% of the recombinants constituting pBS-U21/1530 contained inserts that are present in only one copy in haploid genomic human DNA. Approx. 70% of the sequences mapped to human chromosome 21. Fluorescence in situ hybridization with DNA from pBS-U21/1530 allowed specific, intense staining of the no. 21 chromosomes in metaphase spreads made from human lymphocytes.
ST DNA unique sequence clone selection; sequence DNA low copy repeat clone; human chromosome 21 mapping unique sequence
IT Deoxyribonucleic acid sequences
(unique, method for selecting cloned, from DNA libraries, fluorescence in situ hybridization of human chromosome 21 in relation to)
IT Chromosome
(human 21, unique-sequence DNA on, mapping of, fluorescence in situ hybridization for)
IT Deoxyribonucleic acids
RL: BIOL (Biological study)
(repetitive, low copy no., method for selecting cloned, from DNA libraries, human chromosome 21 in relation to)

L117 ANSWER 19 OF 19 HCAPLUS COPYRIGHT 2003 ACS

AN **1989:89879** HCAPLUS
DN **110:89879**
TI Fluorescence in situ hybridization with human chromosome-specific libraries: detection of trisomy 21 and translocations of chromosome 4
AU Pinkel, D.; Landegent, J.; **Collins, C.**; Fuscoe, J.; Segraves, R.; Lucas, J.; **Gray, J.**
CS Biomed. Sci. Div., Lawrence Livermore Natl. Lab., Livermore, CA, 94550, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1988), 85(23), 9138-42
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
CC 3-5 (Biochemical Genetics)
Section cross-reference(s): 13, 14
AB Chromosomes can be specifically stained in metaphase spreads and interphase nuclei by in situ hybridization with entire chromosome-specific DNA libraries. Unlabeled human genomic DNA is used to inhibit the hybridization of sequences in the library that bind to multiple chromosomes. The target chromosome can be made at least 20 times brighter per unit length than the others. Trisomy 21 and translocations involving chromosome 4 can be detected in metaphase spreads and interphase nuclei by using this technique.
ST human chromosome detection fluorescence hybridization; trisomy 21 detection human fluorescence hybridization; chromosome 4 translocation detection fluorescence hybridization
IT Chromosome
(human 21, trisomy, detection of, by fluorescence in situ hybridization)
IT Nucleic acid hybridization
(in situ, fluorescence, for human trisomy 21 and chromosome 4 translocation detection)
IT Recombination, genetic
(translocation, chromosome 4, of human, fluorescence in situ hybridization for detection of)

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E COLLINS C/AU
L1 807 S E3-E23,E51-E53
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L2 12 S E3-E5
E GRAY J/AU
L3 689 S E3,E30,E31
E GRAY JOE/AU
L4 10 S E3,E4
L5 15 S END SEQUENC?(L)PROFIL?
L6 966 S ESP
L7 1 S L1-L4 AND L5,L6
E SEQUENCE ANALYSIS/CT
E E3+ALL
L8 878518 S E3+NT
L9 734719 S L8 AND PY<=2000
L10 482 S END SEQUENC?
L11 342230 S TERMIN?
L12 292534 S L10,L11 AND PY<=2000
L13 265 S L1-L4 AND L8
L14 235 S L1-L4 AND L9

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L15           1 S L13,L14 AND L10
L16          25 S L13,L14 AND L11
                E COMPUTATION/CT
                E E9+ALL
L17        3603 S E6+NT
L18         531 S L17 AND L9
L19          46 S L17 AND L12
                SEL DN AN 6
L20           1 S E1-E3
L21           3 S L7,L15,L20
                E GENOME/CT
                E E3+ALL
                E E5+ALL
L22       97074 S E4+NT AND L9
                E CHROMOSOM/CT
                E E6+ALL
                E E2+ALL
L23       41888 S E8+NT AND L9
                E E59+ALL
L24        1883 S L9 AND E54+NT
L25        6094 S L9 AND E55+NT
                E CLONE/CT
                E E25+ALL
                E E2+ALL
L26       35529 S E4+NT
                E CLONING, MOLECULAR/CT
                E E3+ALL
L27      117398 S E4+NT
                E E10+ALL
L28        2025 S E9+NT
                E E24+ALL
                E E11+ALL
L29       45092 S E5+NT
                E E23+ALL
L30       32772 S E17+NT
                E E40+ALL
                E E22+ALL
L31       71911 S E4+NT
                E E28+ALL
L32       47762 S E5+NT
L33       31993 S E16+NT OR E17+NT
L34      170652 S L9 AND L26-L33
L35      150092 S L9 AND CLON?
L36      206915 S L34,L35
L37        7716 S L23 AND L36
                E SEQUENCE ANALYSIS+ALL/CT
L38       47793 S E4+NT AND PY<=2000
L39        3546 S L38 NOT AB/FA
L40       44247 S L38 NOT L39
L41          55 S L40 AND L10
L42        9854 S L40 AND L11
                SEL DN AN L41 7 16 28 38 41 44
L43           6 S L41 AND E1-E18
L44           9 S L21,L43 AND L1-L43
L45           9 S L42 AND L17
L46        2105 S L42 AND L22
L47          95 S L42 AND L23
L48          36 S L42 AND L24,L25
L49        3542 S L42 AND L26-L33
L50        3648 S L42 AND CLON?
L51        5342 S L45-L50
L52          95 S L23 AND L51
L53          13 S L52 AND BREAKPOINT
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                E CHROMSOME BREAKAGE/CT
                E CHROMOSOME BREAKAGE/CT
                E E3+LL
                E E3+ALL
L54          864 S E14+NT
L55            2 S L54 AND L51
L56           10 S L51 AND (BREAKPOINT OR BREAK POINT) NOT L53,L55
L57          367 S L51 AND SIZE
L58            2 S L57 AND L10
L59            1 S L58 AND GENOMIC LIBRARY/CT
L60           10 S L44,L59 AND L1-L59
L61            8 S L60 AND CHROMOSOM?
L62           10 S L60 AND (DNA? OR GENOM?)
L63            8 S L60 AND CLON?
L64           10 S L60-L63

     FILE 'MEDLINE' ENTERED AT 16:21:59 ON 15 JUL 2003

     FILE 'BIOSIS' ENTERED AT 16:23:53 ON 15 JUL 2003
                E COLLINS C/AU
L65          754 S E3-E26,E80-E82
                E VOLIK S/AU
L66           16 S E3-E7
                E GRAY J/AU
L67          699 S E3,E40
                E GRAY JOE/AU
L68          140 S E3,E5
L69            2 S E30
L70         1536 S L65-L69
L71            1 S L70 AND L6,L5,L10
L72          695 S L70 AND (CONFERENCE/DT OR 00520/CC)
L73          787 S L70 AND (CONFERENCE OR CONGRESS? OR POSTER OR SYMPOS? OR MEET
L74           93 S L73 NOT L72
L75           67 S L74 NOT ARTICLE/DT
L76          694 S L72 AND L73
L77          695 S L72,L76
L78          309 S (10052 OR 10062 OR 10054 OR 10064)/CC AND L77
L79           25 S L77 AND 04500/CC
L80           21 S L77 AND 00530/CC
L81            9 S L78 AND L79,L80
L82          130 S 03508/CC AND L78
L83            7 S L82 AND L79,L80
L84            7 S L81 AND L83
L85            2 S L81 NOT L84
L86            8 S L71,L84
                SEL DN AN 5-8
L87            4 S L86 NOT E1-E8
L88            4 S L87 AND (10052 OR 10062 OR 10054 OR 10064 OR 03504)/CC

     FILE 'BIOSIS' ENTERED AT 16:41:30 ON 15 JUL 2003
L89           29 S L79,L80 NOT L81,L83-L88
                SEL DN AN L89 12
L90            1 S L89 AND E9-E10
L91          177 S L78 NOT L79-L90
                SEL DN AN 5 7-11 31 40 50
L92            9 S L91 AND E11-E28
L93          357 S L77 NOT L78-L92
                SEL DN AN 3 6 30 31 39 44 60 61 60 70
L94            9 S L93 AND E29-E46
L95           23 S L93 AND COMPAR?(L)GENOM?(L)HYBRID?
L96            7 S L94 AND L95
L97           16 S L95 NOT L96
L98           25 S L94-L97 NOT L88,L90,L92
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     FILE 'HCAPLUS' ENTERED AT 16:53:17 ON 15 JUL 2003
                  E COLLINS C/AU
L99           611 S E3-E27,E126-E132
                  E VOLIK S/AU
L100           22 S E3-E7
                  E GRAY J/AU
L101          205 S E3,E42,E43
                  E GRAY JOE/AU
L102          159 S E3,E5,E6
L103            2 S E65
L104          951 S L99-L103
L105           64 S END SEQUENCE PROFIL?
L106            4 S L104 AND L105
L107          104 S END? SEQUENC? PROFIL?
L108            4 S L104 AND L107
L109            4 S L106,L108
                  SET HIGH ON
L110            4 S L109 AND L99-L109
L111           38 S L99 AND L100-L103
L112           10 S L100 AND L101-L103
L113           10 S L111 AND L112
L114           10 S L110,L113
L115           28 S L111 NOT L114
                  SEL DN AN 3 7 9 10 14 15 25 27 28
L116            9 S L115 AND E1-E27
L117           19 S L114,L116

     FILE 'HCAPLUS' ENTERED AT 17:02:04 ON 15 JUL 2003
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